

WA



RAW SEQUENCE LISTING **ERROR REPORT**

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Application Serial Number: 09/869,486A
Source: P4/09
Date Processed by STIC: 5/14/2002

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FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

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Revised 01/29/2002

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PCT09

RAW SEQUENCE LISTING

DATE: 05/14/2002

PATENT APPLICATION: US/09/869,486A

TIME: 16:27:35

Input Set : A:\B86627026.txt

Output Set: N:\CRF3\05142002\I869486A.raw

Does Not Comply
Corrected Diskette Needed

3 <110> APPLICANT: Scharenberg, Andrew
 5 <120> TITLE OF INVENTION: CHARACTERIZATION OF THE SOC/CRAC CALCIUM CHANNEL PROTEIN
 FAMILY
 7 <130> FILE REFERENCE: B0662/7026/ERP/KA
 9 <140> CURRENT APPLICATION NUMBER: US 09/869,486A
 10 <141> CURRENT FILING DATE: 2002-04-11
 12 <150> PRIOR APPLICATION NUMBER: US 60/114,220
 13 <151> PRIOR FILING DATE: 1998-12-30
 15 <150> PRIOR APPLICATION NUMBER: US 60/120,018
 16 <151> PRIOR FILING DATE: 1999-01-29
 18 <150> PRIOR APPLICATION NUMBER: US 60/140,415
 19 <151> PRIOR FILING DATE: 1999-06-22
 21 <150> PRIOR APPLICATION NUMBER: PCT/US99/29996
 22 <151> PRIOR FILING DATE: 1999-12-20
 24 <160> NUMBER OF SEQ ID NOS: 32
 26 <170> SOFTWARE: PatentIn version 3.0
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 29 <211> LENGTH: 1212
 30 <212> TYPE: DNA
 31 <213> ORGANISM: Homo sapiens
 33 <400> SEQUENCE: 1

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38	tttgagcat ttgtaggaca cagagatagc atggatttac agaggtttaa agaaacatca	180
40	aacaagataa aaatactatc caataacaat acttctgaaa acactttgaa acgagtga	240
42	tctcttgctg gatttactga ctgtcacaga acttccattc ctgttcattc aaaacaagaa	300
44	aaaatcagta gaaggccatc taccgaagac actcatgaag tagattccaa agcagcttta	360
46	ataccggttt gtagatttca actaaacaga tatatattat taaatacatt aaactttttt	420
48	agataagatc tacaaagtgg tgatatttgg gactatatca aaaattcaaa aaaatttttc	480
50	ttaagaaaac tgactttagc atagtagcag ttacagaaaa gtttcttaca gtgaatagtc	540
52	aggaatttta aagaaaaatt tatgcagaat aaaggcagga atctcttttt gtttgaattg	600
54	aagctaatta tatgaactca tttccagcta actgcgataa tgattgattt tgcaaatcc	660
56	ctttaaaaagc acacactgac aagacaaaaa gctcaggaaa aggcaaaaaa attactcctt	720
58	tataatcaag tattatatat aagtcagtgc tcataatttt gctcaagaaa atattgactt	780
60	acattcatat atatctgttc tggcatagag agattatggt gttaaaaatca tgttattgaa	840
62	aaaagttatt tcagtgggga aagagggttag ttaacaaaaga gattcacagt aacaaatcct	900
64	cctttctgga gggactcttc ctgaccctga gctgcacaac tttgcaacaa attaaagcct	960
66	aaccgaagat gacctcaca tggcaattta gaactcatgg gagtcaactt acataaacgg	1020
68	tatttgattt ctgataagat agtggaaatta ttggttatag atgacaaaat aagtatggtt	1080
70	aaagtgatga tggacataaa aaagtttttaa atataaaaaca tgagaaaaaga aggagatact	1140
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78	<211> LENGTH: 141	

*see
pg 3, 6*

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79 <212> TYPE: PRT
 80 <213> ORGANISM: Homo sapiens
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 88 20 25 30
 90 Ala Thr Glu Gly Asp Asn Thr Glu Phe Gly Ala Phe Val Gly His Arg
 91 35 40 45
 93 Asp Ser Met Asp Leu Gln Arg Phe Lys Glu Thr Ser Asn Lys Ile Lys
 94 50 55 60
 96 Ile Leu Ser Asn Asn Asn Thr Ser Glu Asn Thr Leu Lys Arg Val Ser
 97 65 70 75 80
 99 Ser Leu Ala Gly Phe Thr Asp Cys His Arg Thr Ser Ile Pro Val His
 100 85 90 95
 102 Ser Lys Gln Glu Lys Ile Ser Arg Arg Pro Ser Thr Glu Asp Thr His
 103 100 105 110
 105 Glu Val Asp Ser Lys Ala Ala Leu Ile Pro Val Cys Arg Phe Gln Leu
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 130 <222> LOCATION: (29)..(29)
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 139 gactccattt cttcaagcag tctacctctt tgwacagtat atcattatgg ttaatcttct 180
 141 tattgcattt ytcaacaatg tgtatttaca agtgaaggca atttccaata ttgyatggaa 240
 143 gtaccagcgt tatcatttta ttatggctta tcatgagaaa ccagttctgc ctccctccact 300
 145 tatcattctt agccatatag tttctctgtt ttgctgcata tgtaagagaa gaaagaaaga 360
 147 taagacttcc gatggaccaa aacttttctt aacagaagaa gatcaaaaga aacttcatga 420
 149 ttttgaagag cagtgtgttg aaatgtattt caatgaaaaa gatgacaaat ttcattctgg 480
 151 gagtgaagag agaattcgtg tcaacttttga aagagtggaa cagatgtgca ttcagattaa 540
 153 agaagttgga gatccgtgtc aactacataa aaagatcatt acaatcatta gattctcaaa 600
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188 1 5 10 15
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191 20 25 30
W--> 193 Phe Leu Gln Ala Val Tyr Leu Phe Xaa Gln Tyr Ile Ile Met Val Asn
194 35 40 45
W--> 196 Leu Leu Ile Ala Phe Xaa Asn Val Tyr Leu Gln Val Lys Ala Ile
197 50 55 60
W--> 199 Ser Asn Ile Trp Xaa Lys Tyr Gln Arg Tyr His Phe Ile Met Ala Tyr
200 65 70 75 80
202 His Glu Lys Pro Val Leu Pro Pro Pro Leu Ile Ile Leu Ser His Ile
203 85 90 95
205 Val Ser Leu Phe Cys Cys Ile Cys Lys Arg Arg Lys Lys Asp Lys Thr
206 100 105 110
208 Ser Asp Gly Pro Lys Leu Phe Leu Thr Glu Glu Asp Gln Lys Lys Leu
209 115 120 125
211 His Asp Phe Glu Glu Gln Cys Val Glu Met Tyr Phe Asn Glu Lys Asp
212 130 135 140
214 Asp Lys Phe His Ser Gly Ser Glu Glu Arg Ile Arg Val Thr Phe Glu
215 145 150 155 160
217 Arg Val Glu Gln Met Cys Ile Gln Ile Lys Glu Val Gly Asp Pro Cys
218 165 170 175
220 Gln Leu His Lys Lys Ile Ile Thr Ile Ile Arg Phe Ser Asn Trp Pro
221 180 185 190
223 Phe Ala Arg Ser Phe Ser Pro Asp Gly Arg Tyr Ile Lys Asn Thr His
224 195 200 205
226 Trp Pro Lys Ala Ser Glu Ala Ser Lys Val His Asn Glu Ile Thr Arg
227 210 215 220
229 Glu Leu Ser Ile Ser Lys His Leu Ala Gln Asn
230 225 230 235

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Input Set : A:\B86627026.txt

Output Set: N:\CRF3\05142002\I869486A.raw

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254 ttgtaatat ttaatgaaag atgacaaaga tccccagtggt aatataatttg gtcaagacttt      180
256 acctgcagta cccagagaga aagaatttaa ttttccagag gctgggttcct cttctggtgct      240
258 cttattccca agtgcgtgtt cccctccaga actgcgcacag agactacatg gggtagaact      300
260 cttaaaaata tttaataaaa atcaaaaatt aggcagttca tctactagca taccacatct      360
262 gtcattccca csarscaaat tttttgntag tacaccatct cagccaagtt gcaaaaagcca      420
264 cttggaaaact ggaaccaaag atcaagaaac tgtttgctct aaagctacag aaggagataa      480
266 tncagaattt ggagcatttg taggacacag agatagcatg gatttacaga gggtttaaaga      540
268 aacatcaaac aagataaaaa tactatccaa taacaatact tctgaaaaca ctttgaaacg      600
270 agtgagttct cttgctggat ttactgactg tcacagaact tccattcctg ttcattcaaa      660
272 acaagaaaaa atcagtagaa ggccatctac cgaagacact catgaagtag attccaaagc      720
274 agctttaata ccggtttgta gatttcaact aaacagatat atattattaa atacattaaa      780
276 ctttttttaga taagatctac aaagtgggtga tatttgggac tataatcaaaa attcaaaaaa      840
278 atttttctta agaaaactga ctttagcata gtagcagtta cagaaaagtt tcttacagtg      900
280 aatagtcagg aattttaaag aaaaatttat gcagaataaa ggcaggaatc tctttttgtt      960
282 tgaattgaag ctaattatat gaactcattt ccagctaaact gcgataatga ttgattttgc      1020
284 aaattccctt taaaagcaca cactgacaag acaaaaagct caggaaaagg cagaaaaatt      1080
286 actcctttat aatcaagtat tatatataag tcagtgtctc taattttgct caagaaaata      1140
288 ttgacttaca ttcatatata tctgttctgg catagagaga ttatgttggt aaaatcatgt      1200
290 tattgaaaaa agttatttca gtgggggaaag aggttagtta acaaagagat tcacagtaac      1260
292 aaatcctcct ttctggaggg actcttcctg accctgagct gcacaacttt gcaacaaatt      1320
294 aaagcctaac cgaagatgac ctcaaatgg caatttagaa ctcatgggag tcaacttaca      1380
296 taaacgggat ttgatttctg ataagatagt ggaattattg gttatagatg acaaaaataa      1440
298 tatgtttaaa gtgatgatg acataaaaaa gttttaaata taaaacatga gaaaagaagg      1500
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312 <222> LOCATION: (103)..(105)
313 <223> OTHER INFORMATION: any amino acid
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Input Set : A:\B86627026.txt

Output Set: N:\CRF3\05142002\I869486A.raw

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318 <222> LOCATION: (109)..(109)
319 <223> OTHER INFORMATION: any amino acid
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325 <223> OTHER INFORMATION: any amino acid
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333 Asn Pro Phe His Cys Asn Ile Leu Met Lys Asp Asp Lys Asp Pro Gln
334 20 25 30
336 Cys Asn Ile Phe Gly Gln Asp Leu Pro Ala Val Pro Gln Arg Lys Glu
337 35 40 45
339 Phe Asn Phe Pro Glu Ala Gly Ser Ser Ser Gly Ala Leu Phe Pro Ser
340 50 55 60
342 Ala Val Ser Pro Pro Glu Leu Arg Gln Arg Leu His Gly Val Glu Leu
343 65 70 75 80
345 Leu Lys Ile Phe Asn Lys Asn Gln Lys Leu Gly Ser Ser Ser Thr Ser
346 85 90 95
348 Ile Pro His Leu Ser Ser Xaa Xaa Xaa Lys Phe Phe Xaa Ser Thr Pro
349 100 105 110
351 Ser Gln Pro Ser Cys Lys Ser His Leu Glu Thr Gly Thr Lys Asp Gln
352 115 120 125
354 Glu Thr Val Cys Ser Lys Ala Thr Glu Gly Asp Asn Xaa Glu Phe Gly
355 130 135 140
357 Ala Phe Val Gly His Arg Asp Ser Met Asp Leu Gln Arg Phe Lys Glu
358 145 150 155 160
360 Thr Ser Asn Lys Ile Lys Ile Leu Ser Asn Asn Asn Thr Ser Glu Asn
361 165 170 175
363 Thr Leu Lys Arg Val Ser Ser Leu Ala Gly Phe Thr Asp Cys His Arg
364 180 185 190
366 Thr Ser Ile Pro Val His Ser Lys Gln Glu Lys Ile Ser Arg Arg Pro
367 195 200 205
369 Ser Thr Glu Asp Thr His Glu Val Asp Ser Lys Ala Ala Leu Ile Pro
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

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Seq#:4; Xaa Pos. 41,54,69
Seq#:5; N Pos. 387,482
Seq#:6; Xaa Pos. 103,104,105,109,141
Seq#:7; N Pos. 2420,2434,2461,2466,2470
Seq#:9; N Pos. 5094
Seq#:18; N Pos. 6,58,89,406
Seq#:19; Xaa Pos. 15,25,131
Seq#:23; N Pos. 2382,4664,4682,4702,5038,5039,5056,5071,5072
Seq#:24; Xaa Pos. 794
Seq#:26; Xaa Pos. 553,603
Seq#:27; N Pos. 158,6966,6984,7004,7340,7341,7358,7373,7374